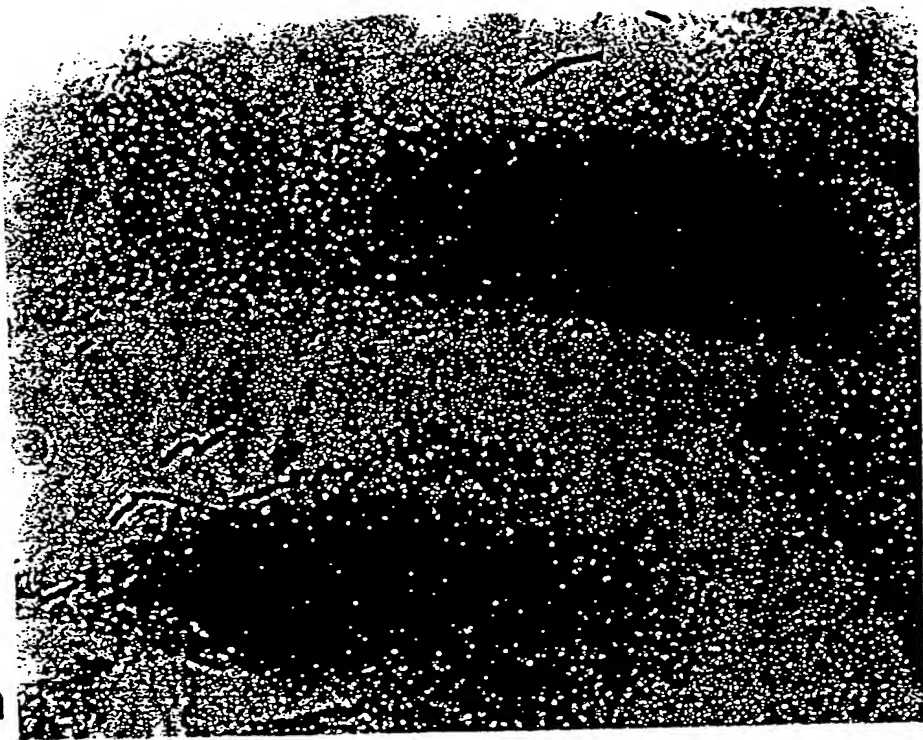


B



A

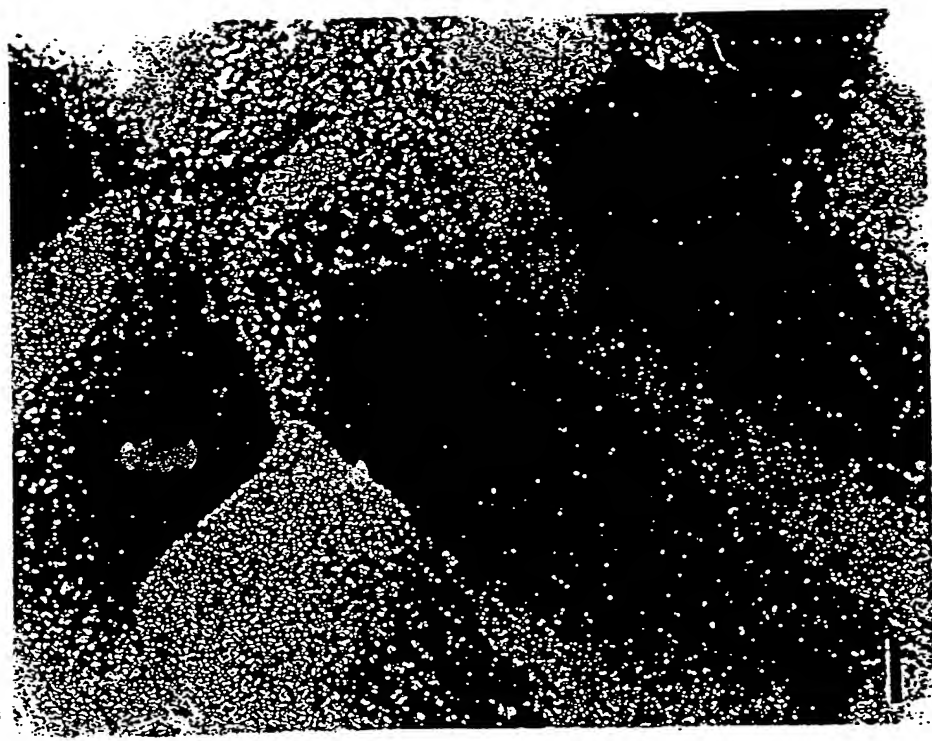


FIGURE 1

FIGURE 2

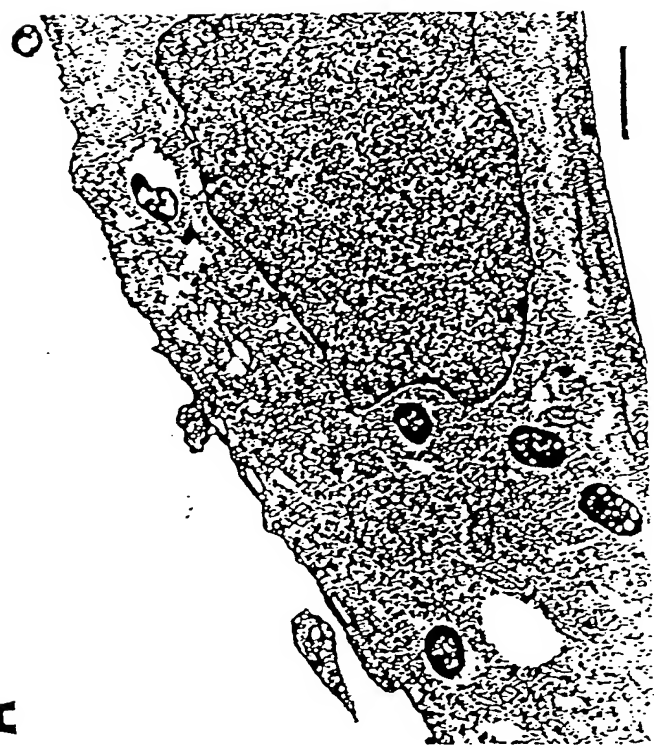
B



D



A



C

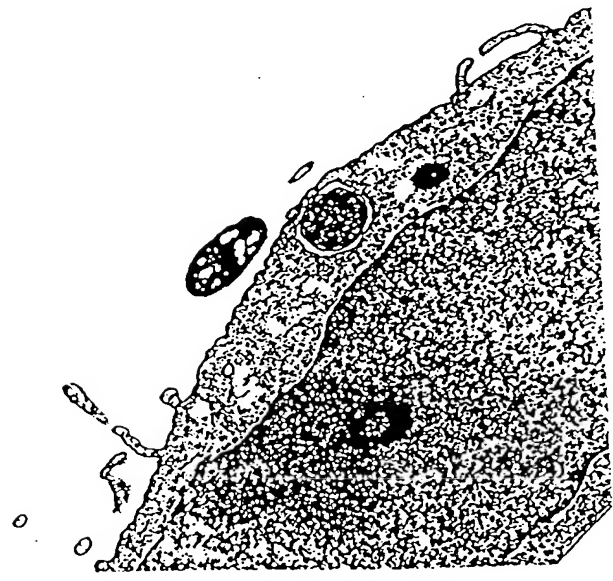


Fig. 3

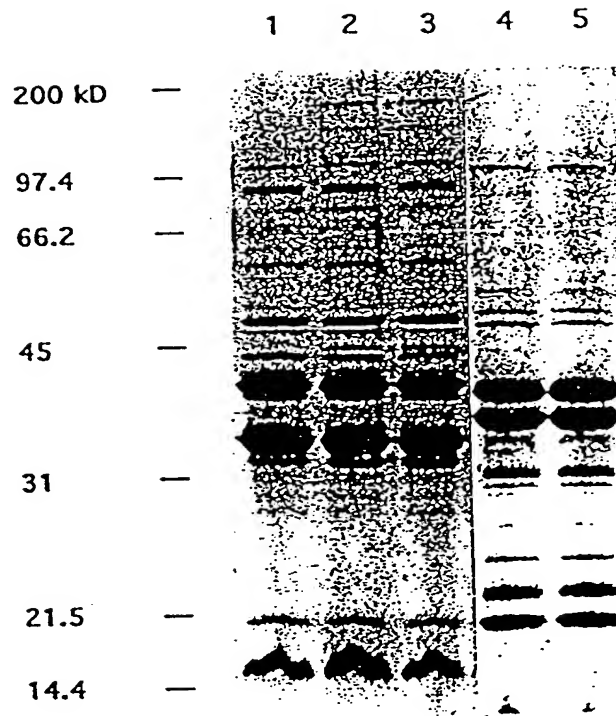


FIGURE 3

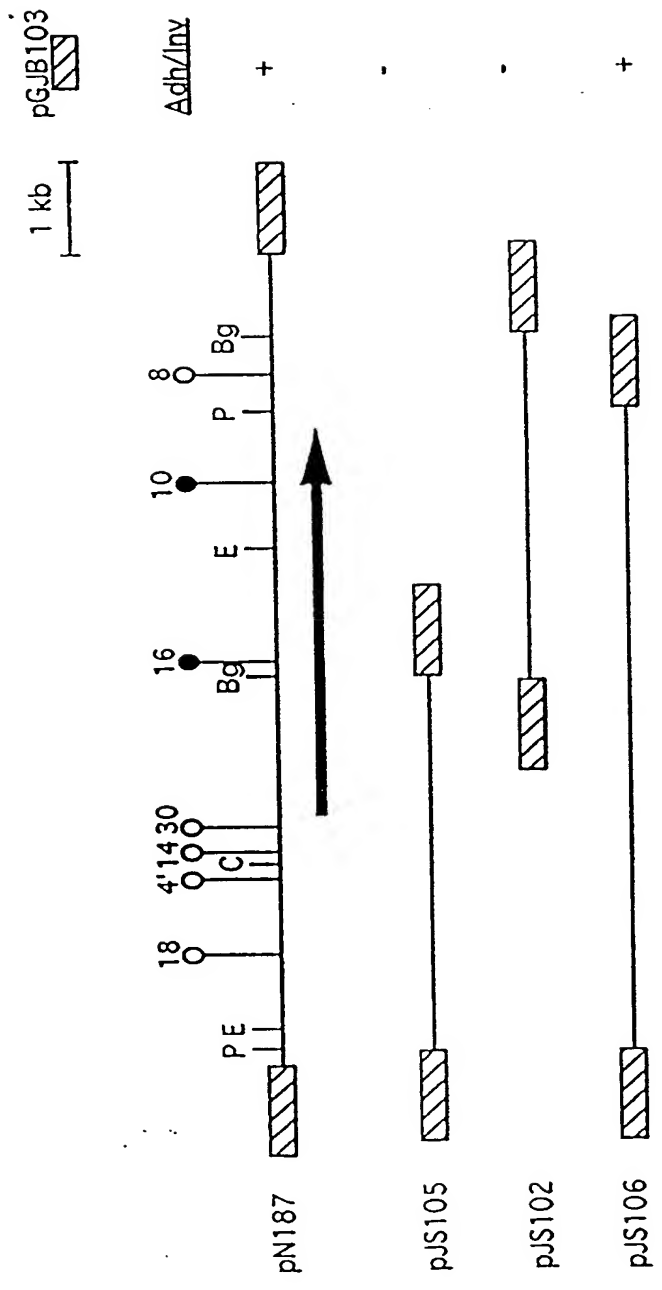


FIGURE 4

Fig. 5

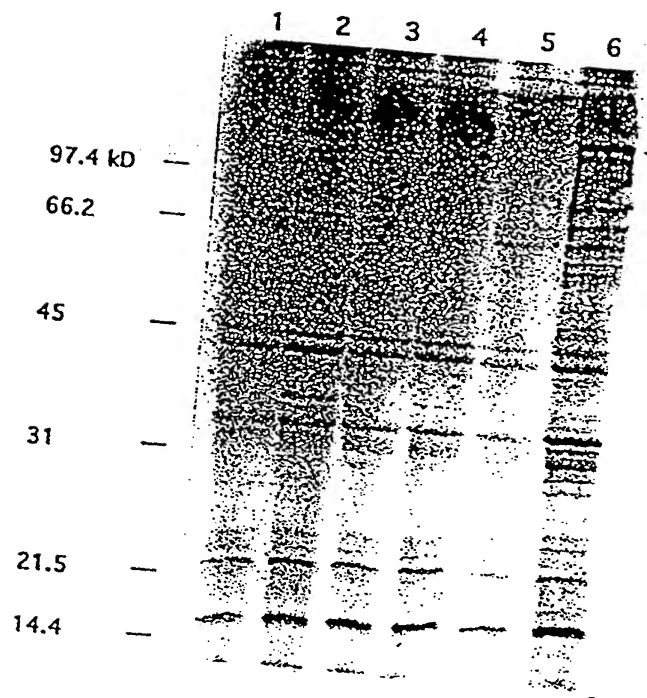


FIGURE 5

10 30 50 70 90
 AATAGTCGTTAACTAGTATTTTTTAAATACGAAAAATTACTTAATTAATAAACATTATGAAAAAACTGTATTTTCGTCTTAATTTT
 -35 -10 M K K T V F R L N F
 110 130 150 170
 AACCGCTTGCATTTTATTAGGGATAGTATCGCAAGCGTGGGCTGGTCACACTTATTTTGGGATTGATTACCAATATTATCGTGATTTT
 T A C I S L G I V S Q A W A G H T Y F G I D Y Q Y Y R D F
 190 210 230 250 270
 CGAGAATAAAGGGAAGTTCACAGTTGGGGCTCAAAATATTAAGGTTTATAACAAACAAGGGCAATTAGTTGGCACATCAATGACAAAA
 E N K G K F T V G A Q N I K V Y N K Q G Q L V G T S M T K
 290 310 330 350
 CCGGATGATTGATTTTCTGTAGTGTACGTAACGGCGTGGCAGCCTTGGTTGAAAATCAATATATTGTGAGCGTGGCACATAACGTA
 P M I D F S V V S R N G V A A L V E N Q Y I V S V A H N V
 370 390 410 430 450
 ATATACAGATGTTGATTTTGGTGCAGAGGGAAACAACCCCGATCAACATCGTTTTACTTATAAGATTGTAACGAAATAACTACAAA
 Y T D V D F G A E G N N P D Q H R F T Y K I V K R N N Y K
 470 490 510 530
 AAGATAATTTACATCCTTATGAGGACGATTACCATAATCCACGATTACATAAATTCGTTACAGAAGCGGCTCCAATTGATATGACTTCG
 D N L H P Y E D D Y H N P R L H K F V T E A A P I D M T S
 550 570 590 610 630
 ATATGAATGGCAGTACTTATTCAGATAGAACAATAATCCAGAACGTGTTTCGTATCGGCTCTGGACGGCAGTTTTGGCGAAATGATCAA
 M N G S T Y S D R T K Y P E R V R I G S G R Q F W R N D Q
 650 670 690 710
 ACAAAGGCGACCAAGTTGCCGGTGCATATCATTATCTGACAGCTGGCAATACACACAATCAGCGTGGAGCAGGTAATGGATATTCGTAT
 K G D Q V A G A Y H Y L T A G N T H N Q R G A G N G Y S Y...
 730 750 770 790 810
 TGGGAGGCGATGTTTCGTAAAGCGGGAGAATATGGTCCATTACCGATTGCAGGCTCAAAGGGGGACAGTGGTTCTCCGATGTTTATTTAT
 G G D V R K A G E Y G P L P I A G S K G D S G S P M F I Y
 830 850 870 890
 ATGCTGAAAAACAAAAATGGTTAATTAATGGGATATTACGGGAAGGCAACCTTTTGAAGGCAAAGAAAAATGGGTTTCAATTGGTTTCGC
 A E K Q K W L I N G I L R E G N P F E G K E N G F Q L V R
 910 930 950 970 990
 AATCTTATTTTATGAAATTTTCGAAAGAGATTTACATACATCACTTTACACCCGAGCTGGTAATGGAGTGTACACAATTAGTGGAAAT
 C S Y F D E I F E R D L H T S L Y T R A G N G V Y T I S G N
 1010 1030 1050 1070
 GATAATGGTCAGGGGTCTATAACTCAGAAATCAGGAATACCATCAGAAATTAATAATTACGTTAGCAAATATGAGTTTACCTTTGAAAGAG
 D N G Q G S I T Q K S G I P S E I K I T L A N M S L P L K E
 1090 1110 1130 1150 1170
 AAGGATAAAGTTCATAATCCTAGATATGACGGACCTAATATTTATTCTCCACGTTTAAACAATGGAGAAACGCTATATTTTATGGATCAA
 K D K V H N P R Y D G P N I Y S P R L N N G E T L Y F M D Q
 1190 1210 1230 1250
 AAACAAGGATCATTAAATCTTCGCATCTGACATTAACCAAGGGGCGGGTGGTCTTTATTTTGGGGTAATTTTACAGTATCTCCAAATTCT
 K Q G S L I F A S D I N Q G A G G L Y F E G N F T V S P N S
 1270 1290 1310 1330 1350
 AACCAAATTTGGCAAGGAGCTGGCATAATGTAAGTGAAGTAAAGTAAATGGCGTGGAAACATGATCGACTTTCT
 N Q T W Q G A G I H V S E N S T V T W K V N G V E H D R L S
 1370 1390 1410 1430
 AAAATTGGTAAAGGAACATTGCACGTTCAAGCCAAAGGGGAAAAATAAAGGTTTCGATCAGCGTAGGCGATGGTAAAGTCATTTTGGAGCAG
 K I G K G T L H V Q A K G E N K G S I S V G D G K V I L E Q

FIGURE 6A

1450 1470 1490 1510 1530
 AGGCAGACGATCAAGGCAACAAACAAGCCTTTAGTGAAATTGGCTTGGTTAGCGGCAGAGGGACTGTTCAATTAAACGATGATAAACAA
 A D D Q G N K Q A F S E I G L V S G R G T V Q L N D D K Q

1550 1570 1590 1610
 TTGATACCGATAAATTTTATTTTCGGCTTTCGTGGTGGTCGCTTAGATCTTAACGGGCATTATTAACCTTTAAACGTATCCAAAATACG
 D T D K F Y F G F R G G R L D L N G H S L T F K R I Q N T

1630 1650 1670 1690 1710
 ACGAGGGGGCAATGATTGTGAACCATAATACAACCTCAAGCCGCTAATGTCACTATTACTGGGAACGAAAGCATTGTTCTACCTAATGGA
 J E G A M I V N H N T T Q A A N V T I T G N E S I V L P N G

1730 1750 1770 1790
 ATAATATTAATAAACTTGATTACAGAAAAGAAATTGCCTACAACGGTTGGTTTGGCGAAACAGATAAAAAATAAACACAATGGGCGATTA
 I N I N K L D Y R K E I A Y N G W F G E T D K N K H N G R L

1810 1830 1850 1870 1890
 AACCTTATTTATAAACCAACCACAGAAGATCGTACTTTGCTACTTTCAGGTGGTACAAATTTAAAGGGCGATATTACCCAAACAAAAGGT
 Y L I Y K P T T E D R T L L L S G G T N L K G D I T Q T K G

1910 1930 1950 1970
 AAACATTTTTTCAGCGGTAGACCGACACCGCACGCCTACAATCATTTAAATAAACGTTGGTCAGAAATGGAAGGTATACCACAAGGCGAA
 K L F F S G R P T P H A Y N H L N K R W S E M E G I P Q G E

1990 2010 2030 2050 2070
 ATTGTGTGGGATCACGATTGGATCAACCGTACATTTAAAGCTGAAAACCTTCCAAATTAAGGCGGAAGTGCGGTGGTTTCTCGCAATGTT
 I V W D H D W I N R T F K A E N F Q I K G G S A V V S R N V

2090 2110 2130 2150
 TCTTCAATTGAGGGAAATTGGACAGTCAGCAATAATGCAATGCCACATTTGGTGTGTGCCAAATCAACAAAATACCATTTGCACGCGT
 S S I E G N W T V S N N A N A T F G V V P N Q Q N T I C T R

2170 2190 2210 2230 2250
 TCAGATTGGACAGGATTAACGACTTGTCAAAAAGTGGATTTAACCGATACAAAAGTTATTAATTCTATACCAAAAACACAAATCAATGGC
 S D W T G L T T C Q K V D L T D T K V I N S I P K T Q I N G

2270 2290 2310 2330
 TCTATTAATTTAACTGATAATGCAACGGCGAATGTTAAAGGTTTAGCAAACTTAATGGCAATGTCACTTTAACAATCAGACCCAATTT
 S I N L T D N A T A N V K G L A K L N G N V T L T N H S Q F

2350 2370 2390 2410 2430
 ACATTAAGCAACAATGCCACCCAAATAGGCAATATTCGACTTTCCGACAATTCAACTGCAACGGTGGATAATGCAAACTTGAACGGTAAT
 T L S N N A T Q I G N I R L S D N S T A T V D N A N L N G N

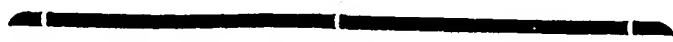
2450 2470 2490 2510
 GTGCATTTAACGGATTAGCTCAATTTTCTTTAAAAAACAGCCATTTTTCGACCAAAATTCAGGGAGACAAAGGCACAACAGTGACGTTG
 V H L T D S A Q F S L K N S H F S H Q I Q G D K G T T V T L

2530 2550 2570 2590 2610
 GAAAATGCGACTTGGACAATGCCTAGCGATACTACATTGCAGAATTTAACGCTAAATAACAGTACGATCACGTTAAATTCAGCTTATTCA
 E N A T W T M P S D T T L Q N L T L N N S T I T L N S A Y S

2630 2650 2670 2690
 GCTAGCTCAAACAATACGCCACGTGCGCGTTTCATTAGAGACGGAACAACGCCAACATCGGCAGAACATCGTTTCAACACATTGACAGTA
 A S S N N T P R R R S L E T E T T P T S A E H R F N T L T V

2710 2730 2750 2770 2790
 AATGGTAAATTGAGTGGGCAAGGCACATTCGAATTTACTTCATCTTTATTTGGCTATAAAAGCGATAAAATTAATAATCAATGACGCT
 N G K L S G Q G T F Q F T S S L F G Y K S D K L K L S N D A

2810 2830 2850 2870
 GAGGGCGATTACATATTATCTGTTGCAACACAGGCAAGAACCCGAAACCTTGAGCAATTAACCTTTGGTTGAAAGCAAAGATAATCAA
 E G D Y I L S V R N T G K E P E T L E Q L T L V E S K D N Q


 — FIGURE 6B —

2890 2910 2930 2950 2970
 CGTTATCAGATAAGCTCAAATTTACTTTAGAAAATGACCACGTTGATGCAGGTGCATTACGTTATAAAATTAGTGAAGAATGATGGCGAA
 L S D K L K F T L E N D H V D A G A L R Y K L V K N D G E

2990 3010 3030 3050
 TCCGCTTGATAACCCCAATAAAAGAGCAGGAATTGCACAATGATTAGTAAGAGCAGAGCAAGCAGAACGAACATTAGAAGCCAAACAA
 R L H N P I K E Q E L H N D L V R A E Q A E R T L E A K Q

3070 3090 3110 3130 3150
 TTGAACCGACTGCTAAACACAAACAGGTGAGCCAAAAGTGCGGTCAAGAAGAGCAGCGAGAGCAGCGTTTCTGATACCCTGCCTGAT
 E P T A K T Q T G E P K V R S R R A A R A A E P D T L P D

3170 3190 3210 3230
 AAAGCCTGTTAAACGCATTAGAAGCCAAACAAGCTGAACTGACTGCTGAAACACAAAAAGTAAGGCAAAAAACAAAAAGTGCGGTCA
 S L L N A L E A K Q A E L T A E T Q K S K A K T K K V R S

3250 3270 3290 3310 3330
 AAAAGAGCAGTGTTTTCTGATCCCCTGCTTGATCAAAGCCTGTTGCGATTAGAAGCCGCACTTGAGGTTATTGATGCCCCACAGCAATCG
 K R A V F S D P L L D Q S L F A L E A A L E V I D A P Q Q S

3350 3370 3390 3410
 GAAAAAGATCGTCTAGCTCAAGAAGAAGCGGAAAAACAACGCAACAAAAAGACTTGATCAGCCGTTATTCAAATAGTGCCTTATCAGAA
 E K D R L A Q E E A E K Q R K Q K D L I S R Y S N S A L S E

3430 3450 3470 3490 3510
 TTATCTGCAACAGTAAATAGTATGCTTTCTGTTCAAGATGAATTAGATCGTCTTTTTGTAGATCAAGCACAATCTGCCGTGTGGACAAAT
 L S A T V N S M L S V Q D E L D R L F V D Q A Q S A V W T N

3530 3550 3570 3590
 ATCGCACAGGATAAAAGACGCTATGATTCTGATGCGTTCGCTGCTTATCAGCAGCAGAAAAACGAACCTTACGTCAAATTGGGGTGCAAAAA
 I A Q D K R R Y D S D A F R A Y Q Q Q K T N L R Q I G V Q K

3610 3630 3650 3670 3690
 GCCTTAGCTAATGGACGAATTGGGGCAGTTTTCTCGCATAGCCGTTGAGATAATACCTTTGATGAACAGGTTAAAAATCACGCGCAATTA
 A L A N G R I G A V F S H S R S D N T F D E Q V K N H A T L

3710 3730 3750 3770
 ACGATGATGTCGGGTTTTGCCCAATATCAATGGGGCGATTTACAATTTGGTGTAACGTTGGGAACGGGAATCAGTGCGAGTAAAATGGCT
 T M M S G F A Q Y Q W G D L Q F G V N V G T G I S A S K M A

3790 3810 3830 3850 3870
 GAAGAACAAAGCCGAAAAATTCATCGAAAAGCGATAAATTATGGCGTGAATGCAAGTTATCAGTTCGTTTAGGGCAATTGGGCATTGAG
 E E Q S R K I H R K A I N Y G V N A S Y Q F R L G Q L G I Q

3890 3910 3930 3950
 CCTTATTTTGGAGTTAATCGCTATTTTATTGAACGTGAAAATTATCAATCTGAGGAAGTGAGAGTGAAAACGCCTAGCCTTGCAATTAAT
 P Y F G V N R Y F I E R E N Y Q S E E V R V K T P S L A F N

3970 3990 4010 4030 4050
 CGCTATAATGCTGGCATTGAGTTGATTATACATTTACTCCGACAGATAATATCAGCGTTAAGCCTTATTTCTTCGTCATTATGTTGAT
 R Y N A G I R V D Y T F T P T D N I S V K P Y F F V N Y V D

4070 4090 4110 4130
 GTTTCAAACGCTAACGTACAAACACGGTAAATCTCACGGTGTTGCAACAACCATTTGGACGTTATTGGCAAAAAGAAGTGGGATTAAAG
 V S N A N V Q T T V N L T V L Q Q P F G R Y W Q K E V G L K

4150 4170 4190 4210 4230
 GCAGAAATTTTACATTTCCAAATTTCCGCTTTTATCTCAAAATCTCAAGGTTCACTCGGCAACAGCAAAATGTGGGCGTGAAATTG
 A E I L H F Q I S A F I S K S Q G S Q L G K Q Q N V G V K L

4250 4270 4290 4310
 GGCTATCGTTGGTAAAAATCAACATAATTTTATCGTTTATTGATAACAAGGTGGGTGAGATCAGATCCCACCTTTTTTATTCCAATAAT
 G Y R W


—  —

FIGURE 6C

	1				50
Hap	MKKTIVFRLNF	LTACISLGI	V SQAWAGHTYF	GIDYQYYRDF	AENKGKFTVG
HK368IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKGKFSVG
HK393IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKGKFSVG
HK715IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKGRFSVG
HK61IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKGKFSVG
Consensus	M---F-LNF	-----	---A-----	--DYQ--RDF	AENKG-F-VG
	51				100
Hap	AQNIVKYNKQ	GQLVGTSMTK	A.PMIDFSV	SRNG.VAALV	ENQYIVSVAH
HK368IGA	ATNVLVKDKN	NKDLGTALPN	GIPMIDFSV	DVDKRIATLI	NPQYVVGVKH
HK393IGA	ATNVEVRDKN	NRPLGNVLPN	GIPMIDFSV	DVDKRIATLV	NPQYVVGVKH
HK715IGA	ATNVEVRDKN	NHSLGNVLPN	GIPMIDFSV	DVDKRIATLI	NPQYVVGVKH
HK61IGA	ATNVEVRDKN	NHSLGNVLPN	GIPMIDFSV	DVDKRIATLV	NPQYVVGVKH
Consensus	A-N--V-K-	---G-----	--PMIDFSV	-----A-L-	--QY-V-V-H
	101				150
HapNVGY	TDVDFGAEQN	NPdqHR....	..FTYKIVKR	NNY.....
HK368IGA	VSNGVSELHF	GNLNGNMNG	NAKAHRDVSS	EENRYFSVEK	NEYPTKLNK
HK393IGA	VSNGVSELHF	GNLNGNMNG	NAKAHRDVSS	EENRYTVEK	NEYPTKLNK
HK715IGA	VSNGVSELHF	GNLNGNMNG	NKSHROVSS	EENRYFSVEK	NEYPTKLNK
HK61IGA	VSNGVSELHF	GNLNGNMNG	NAKSHROVSS	EENRYTVEK	NNFPTENVT
Consensus	-----	-----	N---HR----	----Y--V--	N-----
	151				200
HapKKDNLH	PYEDDYHNPR	LHKFVTEAAP	IDM.TSNMNG	STYSDRTKYP
HK368IGA	TVTTEDQ.TQ	KRREDYMPR	LDKFVTEVAP	IEASTASSDA	GTYNQNKYP
HK393IGA	AVTTEDQ.AQ	KRREDYMPR	LDKFVTEVAP	IEASTDSSTA	GTYNKDKYP
HK715IGA	AVTTEDQ.TQ	KRREDYMPR	LDKFVTEVAP	IEASTASSDA	GTYNQNKYP
HK61IGA	FTTKEEQDAQ	KRREDYMPR	LDKFVTEVAP	IEASTANNK	GEYNNSDKYP
Consensus	-----	---DY--PR	L-KFVTE-AP	I---T-----	--Y----KYP
	201				250
Hap	ERVRIGSGRQ	F.....WRNDQ	DKGDQVAGAY
HK368IGA	AFVRLGSGSQ	FIYKKGDNYS	LIL.....N	NH....EVGG	NNLKLVGDAY
HK393IGA	YFVRLGSGTQ	FIYENGIRYE	LWL.....G	KEGQKSDAGG	YNLKLVGDAY
HK715IGA	AFVRLGSGSQ	FIYKKGDNYS	LIL.....N	NH....EVGG	NNLKLVGDAY
HK61IGA	AFVRLGSGSQ	FIYKKGSRQ	LILTEKDKQG	NLLRNWDVGG	DNLELVGNAY
Consensus	--VR-GSG-Q	F-----	-----	-----	-----V--AY

FIGURE 7A

	251		300
Hap	HYLTAGNTHN QRGAGNGYSY LGG.....D VRKAGEYGPL PIAGSKGDSG		
HK368IGA	TYGLIAGTPYK VNHENNGLIG FGNSKEEHS D PKGILSQDPL TNYAVLGDSD		
HK393IGA	TYGLIAGTPYE VNHENNGLIG FGNSNNEYIN PKEILSKKPL TNYAVLGDSD		
HK715IGA	TYGLIAGTPYK VNHENNGLIG FGNSKEEHS D PKGILSQDPL TNYAVLGDSD		
HK61IGA	TYGLIAGTPYK VNHENNGLIG FGNSKEEHS D PKGILSQDPL TNYAVLGDSD		
Consensus	-Y--AG-----G--G-----PL-----GDSG		*
	301		350
Hap	SPMFYDAEK QKWLINGILR EGNPFEGKEN GFQLVRKSYF D.EIFERDLH		
HK368IGA	SPLFVYDREK GKWLFLGSYD FWAGYN....KKS WQ EWNITYKSQFT		
HK393IGA	SPLFVYDREK GKWLFLGSYD YWAGYN....KKS WQ EWNITYKPEFA		
HK715IGA	SPLFVYDREK GKWLFLGSYD FWAGYN....KKS WQ EWNITYKPEFA		
HK61IGA	SPLFVYDREK GKWLFLGSYD FWAGYN....KKS WQ EWNITYKHEFA		
Consensus	SP-F-YD-EK -KWL--G-----KS--I-----		
	351		400
Hap	TSLYTRAGNG VYTISGNDNG QGSITQKSGI PSEIKITLAN MSLPLKEKDK		
HK368IGA	KDVINKDSAG SLIGSKIDYS WSSNGKTSTI TGGEK....S LNVLDLAD...		
HK393IGA	EKIYEQYSAG SLIGSKIDYS WSSNGKTSTI TGGEK....S LNVLDLAD...		
HK715IGA	KIVLDKDTAG SLTGSNIQYN WNP TGKTSVI SNGSE....S LNVLDLAD...		
HK61IGA	EKIYQQYSAG SLTGSNIQYT WQATGSTSTI TGGE....P LSVLDLAD...		
Consensus	-----G-----S-----S-I-----L-----		
	401		450
Hap	VHNPRYDGEN IYSPRLNNGE TLYFMDQKQG SLIFASDINQ GAGGLYFEGN		
HK368IGAGKD.KPNHGK SVTFEG..SG TLTLNHNIDQ GAGGLFFEGD		
HK393IGAGKD.KPNHGK SVTFEG..SG TLTLNHNIDQ GAGGLFFEGD		
HK715IGASSQD TDSKKNHNGK SVTLRG..SG TLTLNHNIDQ GAGGLFFEGD		
HK61IGAGKD.KPNHGK SITLKG..SG TLTLNHNIDQ GAGGLFFEGD		
Consensus	-----N-G-----G-L-----I-Q GAGGL-FEG-		
	451		500
Hap	FTVSPNSNQ. TWQGAGIHVS ENSTVTWKVN GVEHDRLSKI GKGTILHVQAK		
HK368IGA	YEVKGTSDNT TWKGAGVSVA EGKTVTWKVH NPQYDRLAKI GKGTILVEGT		
HK393IGA	YEVKGTSDNT TWKGAGVSVA EGKTVTWKVH NPQYDRLAKI GKGTILVEGT		
HK715IGA	YEVKGTSDST TWKGAGVSVA DGKTVTWKVH NPKSDRLAKI GKGTILVEGK		
HK61IGA	YEVKGTSDST TWKGAGVSVA DGKTVTWKVH NPKYDRLAKI GKGTILVEGK		
Consensus	--V--S---TW-GAG--V---TVTWKV- ----DRL-KI GKGTIL-V---		


—  —

FIGURE 7B

	501				550
Hap	GENKGSISVG	DGKVILEQQA	DDQGNKQAFS	EIGLVSGRGT	VQLNDDKQFD
HK368IGA	GDNKGSILKVG	DGTVILKQQT	NGSQQ.HAFA	SVGIVSGRST	LVLNDDKQVD
HK393IGA	GDNKGSILKVG	DGTVILKQQT	NGSQQ.HAFA	SVGIVSGRST	LVLNDDKQVD
HK715IGA	GENKGSILKVG	DGTVILKQQA	DANNKVKAFS	QVGIVSGRST	VVLNDDKQVD
HK61IGA	GKNEGLLKVG	DGTVILKQQA	DANNKVKAFS	QVGIVSGRST	LVLNDDKQVD
Consensus	G-N-G--VG	DG-VIL-Q--	-----AF-	--G-VSGR-T	--LNDDKQ-D

	551				600
Hap	TDKIFYGFRG	GRDLINGHSL	TFKRIQNIDE	GAMIVNHNTT	QAANVTITGN
HK368IGA	PNSIYFGFRG	GRDLINGNSL	TFDHIRNIDD	GARLVNHMT	NASNITITGE
HK393IGA	PNSIYFGFRG	GRDLINGNSL	TFDHIRNIDE	GARLVNHSTS	KHSTVTITGD
HK715IGA	PNSIYFGFRG	GRLDANGNLL	TFEHIRNIDD	GARLVNHNTS	KTSTVTITGE
HK61IGA	PNSIYFGFRG	GRDLINGNSL	TFDHIRNIDD	GARVVNHMT	NTSNITITGE
Consensus	----YFGFRG	GRLD-NG--L	TF--I-N-D-	GA--VNH--	-----TITG-

	601				650
Hap	ESIVLPNG..
HK368IGA	SLITDPNTIT	PYNIDAPDED	NPYAFRIKD	GGQLYLNLN	YTTYALRKGA
HK393IGA	NLITDPNNVS	IYYVKPLEDD	NPYAIRQIKY	GYQLYFNEEN	RTYYALKKDA
HK715IGA	SLITDPNTIT	PYNIDAPDED	NPYAFRIKD	GGQLYLNLN	YTTYALRKGA
HK61IGA	SLITNPNTIT	SYNIEAQQDD	HPLRIRSIPY	R.QLYFNQDN	RSYYTLKKGA
Consensus	--I--PN---	-----	-----	-----	-----

	651				700
HapN	NINKLDYRKE	IAYNGWFGET
HK368IGA	STRSELPKNS	GESNENWLYM	GKTSDEAKRN	VMNHINNERM	NGFNGYFGEE
HK393IGA	SIRSEFPQNR	GESNNSWLYM	GTEKADAQKN	AMNHINNERM	NGFNGYFGEE
HK715IGA	STRSELPKNS	GESNENWLYM	GKTSDEAKRN	VMNHINNERM	NGFNGYFGEE
HK61IGA	STRSELPQNS	GESNENWLYM	GRTSDEAKRN	VMNHINNERM	NGFNGYFGEE
Consensus	-----	-----	-----N	--N-----	---NG-FGE-

	701				750
Hap	D.KNKHNGRL	NLIYKPTTED	RTLLISGGTN	LKGDITQIKG	KLFFSGRPTP
HK368IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN	LNGDLTVEKG	TLFLSGRPTP
HK393IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN	LNGDLNVQOG	TLFLSGRPTP
HK715IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN	LNGDLKVEKG	TLFLSGRPTP
HK61IGA	ETKATQNGKL	NVTENGKSDQ	NRFLLTGGTN	LNGDLNVEKG	TLFLSGRPTP
Consensus	--K---NG-L	N-----	---LL-GGTN	L-GD-----G	-LF-SGRPTP


—  —

FIGURE 7C

	751				800
Hap	HAYNHLNKRW	SEMEG..IPQ	GEIVWDHDWI	NRTFKAENFQ	IKGGSADVVS.
HK368IGA	HARDIAGISS	TKKDPHFAEN	NEVVVEDDWI	NRNFKATIMN	VTGNASLYSG
HK393IGA	HARDIAGISS	TKKDSHFSEN	NEVVVEDDWI	NRNFKATININ	VTNNATLYSG
HK715IGA	HARDIAGISS	TKKDQHFAEN	NEVVVEDDWI	NRNFKATININ	VTNNATLYSG
HK611IGA	HARDIAGISS	TKKDPHFTEN	NEVVVEDDWI	NRNFKATIMN	VTGNASLYSG
Consensus	HA-----	-----	-E-V---DWI	NR-FKA----	-----S-
	801				850
Hap	RNVSSIEGNW	TVSNANATF	GVVPNQNTI	CTRSDWTGLT	TCQKVDLIDT
HK368IGA	RNVANITSNI	TASNKAQVHI	GY..KTGDTV	CVRSYDTGYV	TCTIDKLSL
HK393IGA	RNVESITSNI	TASNNAKVHI	GY..KAGDTV	CVRSYDTGYV	TCTIDKLSL
HK715IGA	RNVANITSNI	TASNNAKVHI	GY..KAGDTV	CVRSYDTGYV	TCTIDKLSL
HK611IGA	RNVANITSNI	TASNKAQVHI	GY..KTGDTV	CVRSYDTGYV	TCHNSNLSE.
Consensus	RNV--I--N-	T-S--A----	G-----T-	C-RSD-TG--	TC-----L--
				*	*
	851				900
Hap	KVINSIPKTQ	INGSINLTDN	ATANVKGLAK	LNGNVTLINH	SQFTLSNNAT
HK368IGA	KALNSFNPTN	LRGNVNLTES	A.....
HK393IGA	KALNSFNPTN	LRGNVNLTES	A.....
HK715IGA	KALNSFNATN	VSGNVNLSGN	A.....
HK611IGA	KALNSFNPTN	LRGNVNLTEN	A.....
Consensus	K--NS---T-	--G--NL---	A-----	-----	-----
	901				950
Hap	QIGNIRLSDN	STATVDNANL	NGNVHLTDSA	QFSLKNSHFS	HQIQGDKGIT
HK368IGANEVLGKANL	FGTIQSRGNS	QVRLT.....
HK393IGANEVLGKANL	FGTIQSRGNS	QVRLT.....
HK715IGANEVLGKANL	FGTISGTGNS	QVRLT.....
HK611IGASFTLGKANL	FGTIQSIGTS	QVNLK.....
Consensus	-----	-----ANL	-G-----	Q--L-----	-----
	951				1000
Hap	VTLENATWIM	PSDTTLQNL	LNNSTITLNS	AYSASSNNTP	RRRSLETETT
HK368IGA	...ENSHWHL	TGNSDVHQLD	LANGHIHLNS	ADNSNNVTK.
HK393IGA	...ENSHWHL	TGNSDVHQLD	LANGHIHLNS	ADNSNNVTK.
HK715IGA	...ENSHWHL	TGDSNVNQLN	LDKGHIHLNA	QNDANKVTT.
HK611IGA	...ENSHWHL	TGNSNVNQLN	LINGHIHLNA	QNDANKVTT.
Consensus	---EN--W--	-----L-	L---I-IN-	-----	-----

FIGURE 7D

	1001				1050
Hap	PTSAEHRFNT	LTVNGKLSGQ	GTFQFTSSLF	GYKSDKLKLS	NDAEGDYILS
HK368IGAYNT	LTVNS.LSGN	GSFYLLTDLS	NKQGDQVWVT	KSATGNFTLQ
HK393IGAYNT	LTVNS.LSGN	GSFYLLTDLS	NKQGDQVWVT	KSATGNFTLQ
HK715IGAYNT	LTVNS.LSGN	GSFYLLTDLS	NKQGDQVWVT	KSATGNFTLQ
HK61IGAYNT	LTVNS.LSGN	GSFYWVDFE	NNKSNKVVVN	KSATGNFTLQ
Consensus	-----NT	LTVN--LSG-	G-F-----	-----K----	--A-G---L-

	1051				1100
Hap	VRNTGKEPET	LEQLTLVESK	DNQPLSDKLK	FTLENDHVDA	GALRYKLVKN
HK368IGA	VADKTGEPNH	.NELTLEFAS	KAQR..DHLN	VSLVGNTVDL	GAWKYKLRNV
HK393IGA	VADKTGEPNH	.NELTLEFAS	KAQR..DHLN	VSLVGNTVDL	GAWKYKLRNV
HK715IGA	VADKTGEPTK	.NELTLEFAS	NATR..NNLN	VSLVGNTVDL	GAWKYKLRNV
HK61IGA	VADKTGEPNH	.NELTLEFAS	NATR..NNLE	VTLANGSVDR	GAWKYKLRNV
Consensus	V-----EP--	---LTL----	-----L-	--L---VD-	GA--YKL---

	1101				1150
Hap	DGEFRLHNPI	KEQELHNDLV
HK368IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITIPNN	IQADVPSVPS	NNEELARVDE
HK393IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITIPNN	IQADVPSVPS	NNEELARVDE
HK715IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITIPNN	IQADVPSVPS	NNEELARV.E
HK61IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITIPND	IQADAPSAQS	NNEELARV.E
Consensus	-G---L-NP-	-E-E--N--V	-----	-----	-----


	1151				1200
Hap
HK368IGA	APVPPPAPAT
HK393IGA	APVPPPAPAT
HK715IGA	TPVPPPAPAT
HK61IGA	TPVPPPAPAT	ESAIASEQPE	TRPAETAQPA	MEETNTANST	ETAPKSDTAT
Consensus	-----	-----	-----	-----	-----

	1201				1250
Hap	RAEQAERTLE	AKQVEPT...
HK368IGA	PSETTETVAE	NSKQESKIVE	KNEQDATETT	AQNREVAKA
HK393IGA	PSETTETVAE	NSKQESKIVE	KNEQDATETT	AQNREVAKA
HK715IGA	PSETTETVAE	NSKQESKIVE	KNEQDATETT	AQNGEVAEEA
HK61IGA	QTENPNSESV	PSETTEKVAE	NPPQENETVA	KNEQEATEPT	PQNGEVAKED
Consensus	-----	-----	--Q--T--	-----T--	-----



FIGURE 7E

	1251				1300
HapAKTQT	GE.....
HK368IGA	KSNVKANTQT	NEVAQSGSET	KETQTTETK.ETATVE
HK393IGA	KSNVKANTQT	NEVAQSGSET	KETQTTETK.ETATVE
HK715IGA	KPSVKANTQT	NEVAQSGSET	EETQTTEIK.ETAKVE
HK61IGA	QPTVEANTQT	NEATQSEGKT	EETQTAETKS	EPTESVTVSE	NQPEKTVSQS
Consensus	-----A-TQT	-E-----	-----	-----	-----
	1301				1350
Hap
HK368IGA	KEEK.....
HK393IGA	KEEK.....
HK715IGA	KEEKAKVEKE	EKAKVEKDEI	QEAPQMASET	SPKQAKPAPK	EVSTDTKVVEE
HK61IGA	TEDKVVEKE	EKAKVETEET	QKAPQVTSKE	PPKQAEPAPE	EVPTDTNAEE
Consensus	-----	-----	-----	-----	-----
	1351				1400
Hap
HK368IGA
HK393IGA
HK715IGA	TQVQAQPTQ	STTVAAAEAT	SPNSKPAEET	.QPSEKTNAE	PVTPVWSKNQ
HK61IGA	A..QALQQTQ	PTTVAAAETT	SPNSKPAEET	QQPSEKTNAE	PVTPVVS...
Consensus	-----	-----	-----	-----	-----
	1401				1450
HapPKVRS	RRAARAFFPD	TLP.....
HK368IGAAKVETE	KTQEVPKVTS	QVSPKQEQSE	T.....
HK393IGAAKVETE	KTQEVPKVTS	QVSPKQEQSE	T.....
HK715IGA	TENTTDQPT	REKTAKVETE	KTQEPQVAS	QASPKQEQSE	T.....
HK61IGA	.ENTATQPT	TEETAKVEKE	KTQEVQVAS	QESPKQEOPA	AKPQAQTKPQ
Consensus	-----	-----	-----P-V-S	-----	-----
	1451				1500
Hap
HK368IGAV
HK393IGAV
HK715IGAV
HK61IGA	AEPARENVL	TKNVGEPOPQ	AQPQTQSTAV	PTTGETAANS	KPAAKPQAQA
Consensus	-----	-----	-----	-----	-----


 —————
 FIGURE 7F

	1501			1550
HapD	QSLINALEA.KQAE	TAETQKSKAK TKK.....
HK368IGA	QPQAE	PAREN DPTVNIKEP.QSQT	INT TADTEQPAKE TSSNVE....
HK393IGA	QPQAE	PAREN DPTVNIKEP.QSQT	INT TADTEQPAKE TSSNVE....
HK715IGA	QPQAV	LESEN VPTVNNAEEV	QAQLQTQ	TSA TVSTKQPAPE NSINTG....
HK61IGA	KPQTE	PAREN VSTVNIKEP.QSQT	SA TVSTEQPAKE TSSNVEQPAP
Consensus	-----	---N--E--	-----Q--	T--T-----
	1551			1600
HapV	RSKRAVSDP LLDQSL....
HK368IGAQPVT	ESTTVNTGNS VVEN.....
HK393IGAQPVT	ESTTVNTGNS VVEN.....
HK715IGASAT	AITETAEKSD KPQTETA	AST EDASQHK	ANT VADNSVANNS
HK61IGA	ENSINTGSAT	TMTETAEKSD KPQMET..VT	ENDRQPEANT	VADNSVANNS
Consensus	-----	-----	-----	-----
	1601			1650
HapF	ALEAALEVID	APQQSEKDRL AQEEAEKQRK
HK368IGA	PENTTPATTQ	PTVNSESSN. .KPK.NRHRR
HK393IGA	PENTTPATTQ	PTVNSESSN. .KPK.NRHRR
HK715IGA	ESSEPKSRRR	RSISQPQETS	AEETTAASTD	ETTLADNSKR SKPN.RRSRR
HK61IGA	ESSEKSRRR	RSVSQPKETS	AEETTIVASTQ	ETTVDNSVST PKPERSRTRR
Consensus	-----	-----	-----	-----R-
	1651			1700
HapQKDLI	SRYSNSALSE
HK368IGA	SVRSVPHNVE	PATTSSND..RSTVALCDLT	STNTNAVLSD
HK393IGA	SVRSVPHNVE	PATTSSND..RSTVALCDLT	STNTNAVLSD
HK715IGA	SVRS.....E	PTVINGSD..RSTVALRDLT	STNTNAVLSD
HK61IGA	SVQTNSYEPV	ELPTENAENA	ENVQSGNVA	NSQPALRNLT SKNTNAVLN
Consensus	-----	-----	-----L-	S---N---S-
	1701			1750
Hap	LSA.....TV	NSMLSVQDEL	DRL.FVDQAQ	SAVWTNIAQD KRRYDSDAFR
HK368IGA	ARAKAQFVAL	NVGKAVSQHI	SQLEMNNEGQ	YNVWVSNTSM NKNYSSSQYR
HK393IGA	ARAKAQFVAL	NVGKAVSQHI	SQLEMNNEGQ	YNVWVSNTSM NKNYSSSQYR
HK715IGA	AMAKAQFVAL	NVGKAVSQHI	SQLEMNNEGQ	YNVWVSNTSM NKNYSSSQYR
HK61IGA	AMAKAQFVAL	NVGKAVSQHI	SQLEMNNEGQ	YNVWISNTSM NKNYSSEQYR
Consensus	--A-----	N---V---	--L-----Q	--VW-----
				---Y-S---R

FIGURE 7G

	1751				1800
Hap	AYQQQKTNLR	QIGVQKALAN	GRIGAVFSHS	RSDNTFDEQV	KNHATLTMS
HK368IGA	RFSSKSTQTQ	LGWDQTISNN	VQLGGVFTYV	RNSNNFDKAT	SKN.TLAQVN
HK393IGA	RFSSKSTQTQ	LGWDQTISNN	VQLGGVFTYV	RNSNNFDKAT	SKN.TLAQVN
HK715IGA	RFSSKSTQTQ	LGWDQTISNN	VQLGGVFTYV	RNSNNFDKAS	SKN.TLAQVN
HK611IGA	RFSSKSTQTQ	LGWDQTISNN	VQLGGVFTYV	RNSNNFDKAS	SKN.TLAQVN
Consensus	-----T-----	-----Q-----	-----N-----	-----G-VF-----	-----R--N-FD-----
	1801				1850
Hap	GFAQYQWGD	QF..GVNVGT	GISASKMAEE	QSRKIHRKAI	NYGVNASYQF
HK368IGA	FYSKY.YADN	HWYLGIDLGY	GKFQSKLQTN	HNAKFARHTA	QFGLTAGKAF
HK393IGA	FYSKY.YADN	HWYLGIDLGY	GKFQSKLQTN	HNAKFARHTA	QFGLTAGKAF
HK715IGA	FYSKY.YADN	HWYLGIDLGY	GKFQSNLKTN	HNAKFARHTA	QFGLTAGKAF
HK611IGA	FYSKY.YADN	HWYLGIDLGY	GKFQSNLQTN	NNAKFARHTA	QIGLTAGKAF
Consensus	----Y--D-	----G--G-	G---S-----	---K--R---	--G--A---F
	1851				1900
Hap	RLGQLGIQPY	FGVNRXFIER	ENYQSEEV RV	KTPSLAFNRY	NAGIRVDYTF
HK368IGA	NLGNFGITPI	VGVRYSYLSN	ADFALDQARI	KVNPISVKTA	FAQVDLSYTY
HK393IGA	NLGNFGITPI	VGVRYSYLSN	ADFALDQARI	KVNPISVKTA	FAQVDLSYTY
HK715IGA	NLGNFGITPI	VGVRYSYLSN	ANFALAKORI	KVNPISVKTA	FAQVDLSYTY
HK611IGA	NLGNFAVKPT	VGVRYSYLSN	ADFALAQDRI	KVNPISVKTA	FAQVDLSYTY
Consensus	-IG-----P-	-GV-----	-----R-	K-----	-A-----YT-
	1901				1950
Hap	TPTDNLSVKP	YFFVNYVDVS	NANVQTTVNL	TVLQQPFGRY	WQKEVGLKAE
HK368IGA	.HLGEFSVTP	ILSARY.DAN	QSGSKINVNG	YDFAYNVENQ	QQYNAGLKLK
HK393IGA	.HLGEFSVTP	ILSARY.DAN	QSGSKINVNG	YDFAYNVENQ	QQYNAGLKLK
HK715IGA	.HLGEFSVTP	ILSARY.DTN	QSGSKINVNQ	YDFAYNVENQ	QQYNAGLKLK
HK611IGA	.HLGEFSITP	ILSARY.DAN	QNGSKINVSV	YDFAYNVENQ	QQYNAGLKLK
Consensus	-----S--P	-----Y-D--	-----V--	-----	-Q---GLK--
	1951				1982
Hap	ILHFQISAFI	SKSQGSQIGK	QQNVGVKLG	Y RW	
HK368IGA	YHNVKLSLIG	GLTKAKQAEK	QKTAELKLSF	SF	
HK393IGA	YHNVKLSLIG	GLTKAKQAEK	QKTAELKLSF	SF	
HK715IGA	YHNVKLSLIG	GLTKAKQAEK	QKTAELKLSF	SF	
HK611IGA	YHNVKLSLIG	GLTKAKQAEK	QKTAEVKLSF	SF	
Consensus	-----S---	-----Q--K	Q-----KL--	---	

FIGURE 7H

Fig. 8

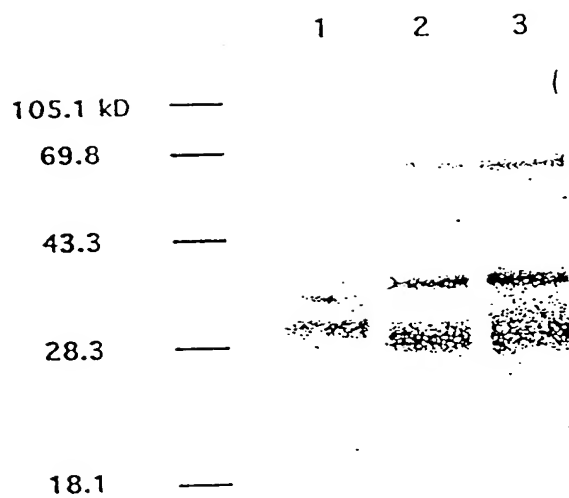
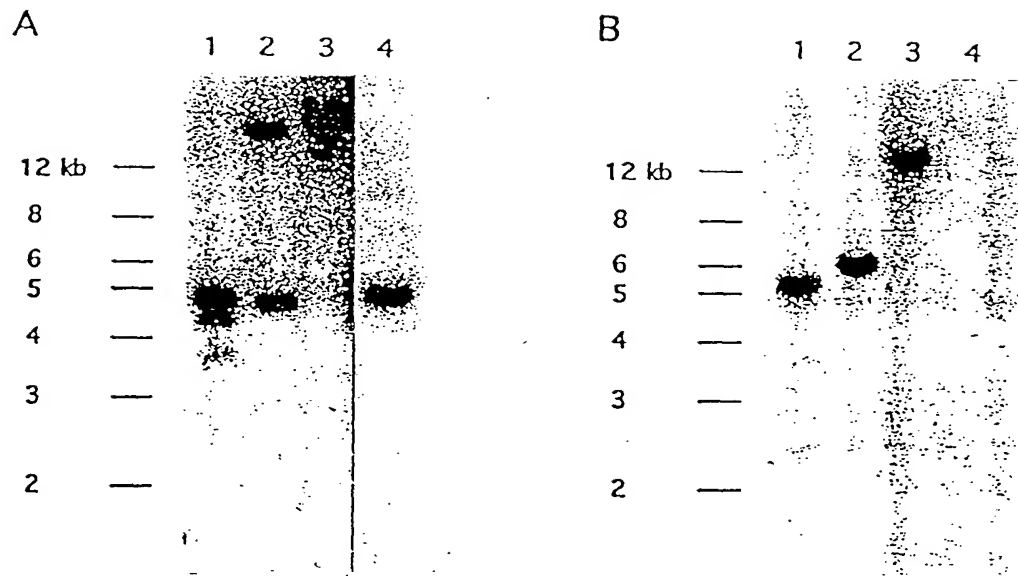


FIGURE 8

Fig. 9



— **FIGURE 9** —

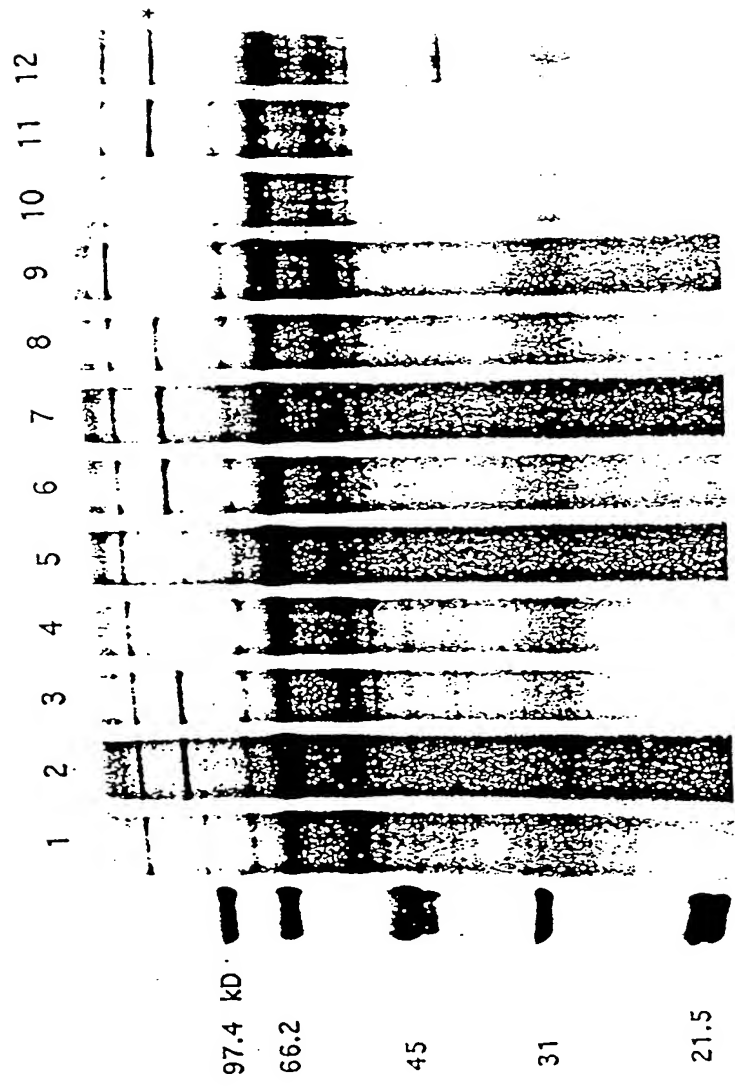


FIGURE 10